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Summary

Freshwater bacterioplankton assemblages are composed of sympatric populations that can be delineated, e.g., by ribosomal RNA gene relatedness and that differ in key ecophysiological properties. They may be free-living or attached, specialized for particular concentrations or subsets of substrates, or invest a variable amount of their resources in defence traits against protistan predators and viruses. Some may be motile and tactic whereas others are not, with far-reaching implications for their respective life styles and niche partitioning. The co-occurrence of competitors with overlapping growth requirements has profound consequences for the stability of community functions; it can to some extent be explained by habitat factors such as the microscale complexity and spatiotemporal variability of the lacustrine environments. On the other hand, the composition and diversity of freshwater microbial assemblages also reflects non-equilibrium states, dispersal and the stochasticity of community assembly processes. This review synoptically discusses the competition and niche separation of heterotrophic bacterial populations (defined at various levels of phylogenetic resolution) in the pelagic zone of inland surface waters from a variety of angles, focusing on on habitat heterogeneity and the resulting biogeographic distribution patterns, the ecophysiological adaptations to the substrate field, and the interactions of prokaryotes with predators and viruses.

Introduction:

Heterotrophic microorganisms in limnic systems are responsible for most cycling of organic matter and for the larger part of system respiration (Cole et al., 2000). The comparative analysis of marker genes has revealed that there is indeed a distinct set of 'freshwater-specific' bacterial taxa from various phylogenetic lineages (Zwart et al., 2003; Warnecke et al., 2004; Newton et al., 2011). Such genotypes are likely seeded into streams, rivers and lakes from the terrestrial realms, where they may be present in very low abundances (Ruiz-González et al., 2015). Sequence analysis of rRNA genes also shows that there are complex association networks within freshwater microbial assemblages, possibly indicative of competitive relationships and niche separation. Distinct sets of bacterial genotypes tend to significantly co-occur in lacustrine habitats (Chaffron et al., 2010; Eiler et al., 2012); their co-occurrence patterns suggest consistent temporal differences of community complexity (Kara et al., 2013), i.e., periods with potentially more or less pronounced microbial interactions. The topologies of the so constructed networks also point to subsets of disproportionally well-connected or centrally positioned taxa ('hubs' and 'bottlenecks') that might play a prominent role in overall community stability (Peura et al., 2015).

However, while it is intuitively attractive to synoptically assess the relationships between all members of lacustrine microbial assemblages at once (Tsai et al., 2015), the so revealed statistical correlations are causally often rather ambiguous. A conspicuous temporal co-occurrence of genotypes may indicate both, fierce competition or the lack thereof (total niche separation), but might also be due to dispersal patterns within larger metacommunity systems (Crump et al., 2007; Lindström and Langenheder, 2012), e.g., influx from the catchment (Ruiz-González et al., 2015; Niño-Garcia et al., 2016a). Thus, in order to understand and properly interpret community level patterns derived from sequence analysis, it is also necessary to experimentally study the interactions between individual bacterial strains and populations, between bacterial taxa and their predators and parasites, and their separation by various environmental drivers and conditions. In this context, the niches of the various freshwater bacterioplankton taxa can be looked upon from a variety of angles, such as their ecophysiological differences, their respective distributions in time and space within a particular system, or their biogeographic occurrence patterns across a 'landscape' of lacustrine habitats with contrasting physicochemical properties. While the most appropriate objects of such autecological examination would be populations of validly defined species or unique genotypes (Choudoir et al., 2012), it is often not possible to properly delineate such units in field studies, which, in turn, are the life blood of environmental microbiology. Thus, my review will mix information from various taxonomic ranks, and I shall frequently resort to presenting findings about rather ill-defined taxa (i.e., the somewhat ephemeral 'operational

taxonomic units' [OTUs] derived from the -comparatively crude- distance-based clustering of partial rRNA gene sequences) (Edgar, 2013).

Recently, Šimek and co-workers have referred to the factors controlling the development of the spring microbial assemblages as a 'finely tuned symphony' (Šimek et al., 2014). My own metaphor for the relationship of pelagic bacteria with each other and their environment would be Augusto Boal's 'invisible theater' that plays out on improvised stages and suspends the distinctions between protagonists, chorus and spectators (Boal, 2000). Accordingly, this review attempts to synoptically address a variety of facets that are deemed relevant to understand the genomically 'scripted' and the 'spontaneous' interactions between pelagic freshwater microbes and the resulting patterns of community structure and functioning. While my focus is largely limited to freshwater bacteria, I occasionally refer to studies from other environments to illustrate concepts that have not yet been properly tested in lacustrine habitats.

Selection-driven vs. stochastic community assembly

The microbes that thrive in the freshwater pelagic zone are probably not just a random collection of genotypes from neighbouring habitats or biomes, as was assumed by early microbiologists (Jordan, 1918). However, in ecological analogy with Gould's critique of the 'Panglossian' evolutionary paradigm (Gould and Lewontin, 1979), one should not resort too confidently to Baas-Becking's postulate on the 'selecting environment' (Baas-Becking, 1934) to explain the site-specific accumulation or co-occurrence of particular microbial genotypes. The assembly of local communities from a regional species pool is simultaneously driven by stochastic effects such as immigration and drift ('mass effects') and deterministic factors, also known as 'environmental filtering' or 'species sorting' (Leibold et al., 2004; Lindström and Langenheder, 2012; Nemergut et al., 2013). There is substantial disagreement between 'neutral' and 'niche-based' theory as to which of these processes may be more important for defining local community composition (Chase and Myers, 2011), and their respective contributions might be difficult to resolve: High diversity between local assemblages (i.e., beta diversity) might be explained by the action of local selective factors and intermediate dispersal rates (Declerck et al., 2013). However, a similar pattern might also form due to stochasticity at identical habitat conditions, e.g., caused by historical, 'priority' effects that favour early arriving genotypes (Andersson et al., 2014). Both, abiotic parameters (low pH) and ecological interactions (predation) have been shown to shift the balance of community assembly mechanisms towards species sorting (Chase et al., 2009; Ren et al., 2015). By contrast, higher productivity appears to change these processes towards stochasticity, resulting in greater beta

diversity at comparable conditions (Chase, 2010). In the extreme, even identical environmental constraints can lead to the formation of microbial communities with distinct genotypic composition that all originate from a single inoculum; these communities may, moreover, differ in functional properties (Zhou et al., 2013).

Biogeographic distribution patterns and habitat selection

The science of biogeography seeks to understand the spatial distribution patterns of organisms by synoptically assessing the relative importance of the above described factors, i.e., historic events vs. contemporary environmental conditions. In view of the high potential dispersal rates of free-living microbes, the existence of 'true' microbial biogeography as shaped by geographic barriers has been subject of debate (Finlay, 2002; Whitaker et al., 2003; Foissner, 2006). A comprehensive review of various aspects of microbial biogeography is provided by Martiny et al (Martiny et al., 2006).

Dispersal doubtlessly plays a key role in shaping the composition of freshwater bacterioplankton assemblages (Nelson et al., 2009; Lindström and Langenheder, 2012), and hydrological processes within the catchment are major determinants for the structuring of lacustrine metacommunities (Crump et al., 2007; Ruiz-González et al., 2015; Niño-Garcia et al., 2016a). Moreover, an interplay of stochastic and deterministic factors might act on different components of aquatic microbial assemblages: A study in Chinese lakes suggests that rare genotypes were more strongly selected by local environmental conditions, whereas regional factors were more important in determining the occurrence patterns of the dominant genotypes (Liu et al., 2015). A somewhat contrasting conclusion was reached in a boreal lake and river system, i.e., communities were composed of a subset of locally selected abundant 'competitive winners' and of a diverse mix of rare 'dispersers' introduced from the catchment (Niño-Garcia et al., 2016b). A part of this apparent contradiction may be due to the problematic nature of the 'rare' vs. 'abundant' categories; for one, the involved methods are at best semi-quantitative, and secondly, a single sample may not be a sufficiently solid base to assess the highly fluctuating population sizes of the more 'opportunistically' growing bacterial populations (Shade et al., 2014; Lynch and Neufeld, 2015).

Notwithstanding neutral community assembly mechanisms only a subset of the global diversity of lake bacterioplankton is found in any given system (Livermore and Jones, 2015). There is evidence for the sorting of freshwater bacterial taxa (approximately genus-level rRNA-defined OTUs) according to local conditions (Van der Gucht et al., 2007), such as pH or salinity (Logares et al., 2013; Niño-Garcia et al., 2016a), as well as for the physiological adaptation of ecotypes (strains of the same species) from freshwater and

hypersaline ponds to their geographic origin (Hahn and Pöckl, 2005; Rossello-Mora et al., 2008). For example, the increase of water residence time may lead to reduced bacterial richness (Niño-Garcia et al., 2016a), suggesting a shift of assembly processes towards local selection (Lindström et al., 2005). At the community level, such 'species' sorting is, e.g., reflected in the distribution of microbial rRNA genotypes across high mountain lakes (Sommaruga and Casamayor, 2009), or in the relationship between their richness and nutrients in oligotrophic systems (Logue et al., 2012). The concept of selection by local environmental factors also holds true for individual taxa within the numerically important freshwater bacterioplankton lineages: Different phylogenetic clades (i.e., genera-like 'tribes') of *Actinobacteria* were distributed across lakes in correspondence with their physicochemical properties rather than their geographic distance (Newton et al., 2007). *Betaproteobacteria* affiliated with the genera *Limnohabitans* and *Polynucleobacter* had contrasting abundance patterns in lakes with high and low pH, respectively (Jezbera et al., 2012), and the biogeographic distribution of two species-like taxa of filamentous *Saprospiraceae* from the LD2 lineage (Candidatus Aquirestis calciphila and Candidatus Haliscomenobacter calcifugiens) (Hahn and Schauer, 2007) could be readily explained by water hardness (Schauer et al., 2005). Studies at higher taxonomic resolution have, moreover, revealed variability of environmental preferences within single genera (Jezbera et al., 2013) which likely reflects the ecophysiological differences between species (Hahn et al., 2011a; Hahn et al., 2011b; Kasalický et al., 2013). In fact, ecologically relevant adaptations may not even be imprinted on the slowly evolving ribosomal genes at all, as in the case of optimal growth temperatures of actinobacterial strains isolated from different geographic regions (Hahn and Pöckl, 2005). The physiological reason for such acclimation may be subtle, e.g., an altered composition of the cell membrane (Hall et al., 2010). The betaproteobacterial freshwater genus *Polynucleobacter* harbours several free-living species that are so closely related that the have been regarded as subspecies until recently (Hahn et al., 2009; Hahn et al., 2016b). These species nevertheless show conspicuous ecological diversification (Jezberova et al., 2010; Jezbera et al., 2011), e.g., with respect to pH, chromophoric dissolved organic carbon (DOC, i.e., humic substances) and alkalinity. Two species with evidently contrasting habitat preferences, *P. asymbioticus* and *P. duraque*, display genomic specialization for transporters of ferrous vs. ferric iron, respectively (Hahn et al., 2016a), in accordance with the bioavailability of these iron species in acidic and alkaline freshwater systems.

Competition is important for community stability

The relationship between biodiversity, environmental heterogeneity and the stability of natural communities has intrigued ecologists since many decades (Hutchinson, 1959; May, 1973). I draw the reader's attention to the concise historical review by McCann on the overall debate on the relationship between diversity and stability (McCann, 2000).

The co-occurrence of competitors in microbial assemblages is believed to be beneficial for overall community stability: The concept of 'functional redundancy' refers to the presence of sympatric populations with overlapping traits and requirements, so that the extinction of one such population would lead to the rise of a competing one with a comparable functional role (Allison and Martiny, 2008; Shade et al., 2012). This is regarded as one possible 'insurance' for the stability of fundamental processes (e.g., degradation or biomass production) upon disturbance or environmental change, i.e., their uncoupling from compositional shifts within microbial assemblages (Werner et al., 2011; Langer et al., 2015). For example, while the total microbial uptake of N-acetyl glucosamine remained rather stable over the course of a spring phytoplankton bloom in a mesotrophic lake, there was a pronounced shift in the composition of the bacterial taxa (at the approximate level of genera) that consumed this compound (Eckert et al., 2012). The high diversity of natural freshwater microbial assemblages (Logue et al., 2012; Livermore and Jones, 2015), the disproportionally high co-occurrence of phylogenetically closely related rRNA-defined genotypes (e.g. within *Chitinophagaceae* or acI actinobacteria) (Comte et al., 2016) and the stability of microbial processes such as the turnover of labile organic substrates despite rapid community changes (Weiss and Simon, 1999; Eckert et al., 2012) together are indicative for the presence of numerous functionally redundant ecotypes in such habitats. Many of these populations may be small or dormant at any given time, but might be rapidly re-activated at favourable conditions or after a disturbance event (Piccini et al., 2006; Fazi et al., 2008; Shade et al., 2014; Neuenschwander et al., 2015).

However, Bisset et al (Bissett et al., 2013) have pointed out that there may be no single 'optimum state' for a microbial assemblage to which it would tend to return by resilient processes (Shade et al., 2012), and that different community states 'may […] exist despite communities being assembled under similar environmental conditions'. Moreover, the classifying of genotypes as being 'functionally redundant' is an operational procedure that is only valid within a particular environmental scenario; a change in growth conditions may well lead to a role change of so-called functionally redundant (competing) taxa into functionally complementary (cooperating) ones (Fetzer et al., 2015). In addition, bacterial communities as a whole, but also individual genotypes (even at the level of individual strains) may greatly differ in their metabolic or phenotypic plasticity, i.e., they physiologically acclimate to particular scenarios such as increasing substrate levels (Hahn et al., 2004; Comte et al., 2013) or the presence of predators (Corno and Jurgens, 2006; Blom et al., 2010). This trait is regarded to

be particularly advantageous at instable environmental conditions, while more stable environments tend to select for genotypic specialization (Yamamichi et al., 2011). At an ecosystem level, phenotypic plasticity of individual populations has thus been proposed to increase community wide 'resilience' or 'resistance' to environmental change (Bernhardt and Leslie, 2013). A comprehensive analysis across numerous freshwater habitats concluded that community-level metabolic plasticity appeared to be an intrinsic emergent property of aquatic microbial assemblages. Moreover, it was tightly coupled to functional redundancy, suggesting a positive selection for co-occurring genotypes with high individual metabolic flexibility (Comte et al., 2013).

Habitat variability creates niche space

Freshwater microbes appear to thrive in an unstructured environment that is largely homogeneous with respect to substrate distribution. However, physical, biogeochemical and biological factors superimpose structure onto pelagic habitats at various spatial and temporal scales (Allgaier and Grossart, 2006; Shade et al., 2008). This heterogeneity may be relevant for bacterial assemblages in the productive surface water layers, as it likely mediates the co-existence of genotypes with contrasting growth strategies. While the temporal aspect of variability, in particular seasonality (e.g., (Allgaier and Grossart, 2006)), is probably the more well-studied one, spatial heterogeneity has also attracted considerable attention, e.g., in systems with pronounced vertical oxygen gradients (Overmann et al., 1999; Peura et al., 2012), along lake-wide longitudinal scales (Salcher et al., 2011b), or with respect to their fine-scale horizontal variability patterns (Lear et al., 2014).

Microbial succession patterns share certain features with those of higher organisms, but there are also key differences such as the more prominent role of persistence, metabolic diversity, or contemporary evolutionary processes (Fierer et al., 2010). The temporal variability that affects aquatic microbial populations and communities in lakes spans from less than hours to years: Microbial activity patterns and population dynamics respond to substrate or nutrient pulses (Newton and McMahon, 2011; Canelhas et al., 2016) and to diel change (Vila-Costa et al., 2013), and individual rRNA-defined populations of free-living bacteria may wax or wane within days (Piccini et al., 2006; Eckert et al., 2012; Shade et al., 2014; Šimek et al., 2014) due to changes in top-down or bottom-up control factors (Šimek et al., 2005; Neuenschwander et al., 2015). Recurrent or stochastic seasonal events, such as changes in phytoplankton composition (Paver et al., 2015), cyanobacterial blooms (Eiler and Bertilsson, 2004) or their breakdown (Bizic-Ionescu et al., 2014), and even typhoons (Jones et al., 2008) may trigger succession patterns or select for particular sets of genus-like taxa. This has been mainly

shown for planktonic bacteria (Kent et al., 2004; Schauer et al., 2006; Wu and Hahn, 2006; Salcher et al., 2008; Salcher et al., 2011a; Eiler et al., 2012), but also seems to hold true for the particle-attached microbial assemblages (Rösel et al., 2012; Datta et al., 2016).

Spatial variability of the physicochemical environment, and of microbial abundances, activity, or community composition is found at scales that range from less than a millimetre to kilometres (Seymour et al., 2004; Salcher et al., 2011b; Stocker, 2012; Lear et al., 2014), or, in the case of rivers, hundreds of kilometres (Read et al., 2015; Savio et al., 2015). Even the top surface (neuston) layer of small waterbodies represents a distinct habitat that selects for a specifically adapted microflora (Stürmeyer et al., 1998; Hörtnagl et al., 2010). At the lowest end of the size spectrum, heterogeneity is generated by various ecological and physicochemical processes, not least by the microorganisms themselves: Phytoplankton cells may be surrounded by a 'phycosphere' of elevated concentrations of organic compounds that attract chemotactic bacteria (Bell and Mitchell, 1972), and macroscopic organic particles are formed in lakes by aggregation of senescent phytoplankton cells and other types of debris (Grossart and Simon, 1993). The patchy and discontinuous distribution of phyto- and zooplankton populations (Pinel Alloul et al., 1995; Reynolds, 2006) superimposes another layer of biological variability at a larger scale. In addition, physical structuring of the surface water column may occur at scales of centimetres to meters, e.g., due to turbulent mixing (Wuest and Lorke, 2003), thermal stratification or light transparency, and at kilometre scales due to basin morphology (Armengol et al., 1999) or other hydrological properties. Such processes might in fact translate the patchiness of substrate concentrations that is biologically generated at a micro- and mesoscale into larger, eventually system-wide patterns of heterogeneity (Horňák et al., 2016). The most obvious system-wide spatial pattern in deep, thermally stratified lakes is a clear distinction between the microbial assemblages in the oxygenated epi- and hypolimnetic realms (Okazaki et al., 2013; Okazaki and Nakano, 2016): Various groups of photoheterotrophic bacteria featuring light-harvesting pigments are typical for the upper, photic zone (Atamna-Ismaeel et al., 2008; Sharma et al., 2009; Martinez-Garcia et al., 2012), whereas the deeper zones harbour microbial taxa with distinct physiological traits that are rare or absent in the surface layers, such as *Chloroflexi* (Denef et al., 2016), *Thaumarchaeota* (Callieri et al., 2009; Berdjeb et al., 2013; Coci et al., 2015) or methylotrophs (Salcher et al., 2015).

Attached bacteria

Suspended organic aggregates play a crucial role in freshwater environments both, as microbial habitats and as point sources of readily degradable labile DOC (Grossart and Simon,

1998; Stocker, 2012). The particle-attached bacterial assemblages communities overlap to some extent with the planktonic ones, as deduced from 16S rRNA fingerprinting (Rösel et al., 2012), but are nevertheless distinct (Parveen et al., 2011) even at the phylum level (Schmidt et al., 2016). Moreover, they are specific for lacustrine systems (Bizic-Ionescu et al., 2015) and differ from the free-living community in their response to major ecological drivers (e.g., phytoplankton blooms) (Rösel and Grossart, 2012). Attached bacteria are of key importance for the degradation of macromolecules and the subsequent release of labile organic matter into the surrounding water (Grossart et al., 2007). Following an initial colonization phase (Kiorboe et al., 2002), the attached communities settle into a dynamic equilibrium of attachment and detachment (the 'swim-or-stick' lifestyle), and their densities are increasingly determined by growth processes (Grossart et al., 2003). In fact, the decision if and when to detach and explore may in itself represent a distinguishing trait between otherwise identical genotypes (Yawata et al., 2014). It has been argued that the close physical associations between populations of attached microbes will strongly select for interaction-driven community dynamics (Grossart et al., 2003; Cordero and Datta, 2016), e.g. with respect to communication (Gram et al., 2002), metabolic complementarities (Beier and Bertilsson, 2013; Garcia et al., 2015), parasitism (Jagmann et al., 2010), or antagonism (Grossart et al., 2004). In fact, the very formation of aggregates (Corno et al., 2013) and the degradation of complex polymeric substrates (Beier and Bertilsson, 2013; Corno et al., 2015) can be the result of cooperative interaction between species, resulting in reproducible succession patterns on aging particles (Datta et al., 2016). Besides algal-derived organic aggregates, freshwater microbes will also colonize other available surfaces, in particular the zooplankton (Tang et al., 2010). This 'hitch hiking' provides bacteria with a means of increasing their dispersal (Grossart et al., 2010), and, in turn, is also beneficial to their hosts (Sison-Mangus et al., 2015; Peerakietkhajorn et al., 2016). Moreover, the consumption of zooplankton together with their attached microflora by fish may represent a shortcut within microbial food webs that increases DOC transfer efficiency by several orders of magnitude (Eckert and Pernthaler, 2014).

Motile vs. non-motile lifestyles

The by far largest part of the pelagic zone of lakes remains the realm of the planktonic microbes, which may be at least as numerous and productive as their attached counterparts (Middelboe et al., 1995). Free-living bacteria can be broadly categorized into motile and non-motile forms that likely differ in their ecophysiological adaptations to locally variable substrate levels: Motile cells can track gradients of organic compounds and are thus expected to interpret a rise of substrate concentrations as a signal for increasingly favourable growth

conditions. By contrast, non-motile bacteria are passively exposed to the stochastic variability of the substrate field (Horňák et al., 2016) from which they cannot predict the growth conditions in their immediate future. They should, therefore, exhibit a much more limited physiological response to substrate heterogeneity or gradients (Fig. 1). This might in fact be one reason why important taxa of non-motile bacteria such as the order-like lineage of acI actinobacteria, harbouring the Candidatus genus Planktophilia (Jezbera et al., 2009) or LD12 alphaproteobacteria from the candidate order Pelagibacteriales (also known as the freshwater SAR11-IIIb lineage) still resist all cultivation attempts (Ghylin et al., 2014; Eiler et al., 2016), while other predominantly non-motile genera such as *Polynucleobacter* spp. require prolonged acclimation to elevated substrate levels before they can be isolated (Hahn et al., 2004; Hahn et al., 2012).

Motile freshwater bacteria comprise well-studied cultivable genera such as *Caulobacter, Aeromonas, Acidovorax*, or *Massilia*. Motility is characteristic of the free-living lifestyle of many bacteria that also attach to surfaces (Kiorboe et al., 2002). It is lost upon attachment, but also as a response to starvation (Morita, 1997). Motility is the precondition for a tactic response to environmental gradients; it forms the link between planktonic microbial cells and the scarce organic particles in pelagic habitats (Kiorboe et al., 2002), as only motile cells can directly capitalize on such microscale resource patchiness (Kiorboe and Jackson, 2001; Stocker et al., 2008; Stocker, 2012; Taylor and Stocker, 2012). Motile aquatic bacteria may sense organic compounds already at low nM concentrations, and the parallel presence of high and-low affinity uptake systems allows for the efficient exploitation of large differences in substrate levels (Geesey and Morita, 1979). It has been argued that motile bacteria may entirely meet their carbon demand by travelling from one organic particle to another or by tracking the 'wakes' of compounds released during the sinking of aggregates (Kiorboe and Jackson, 2001). Up to 70% of pelagic bacteria in coastal sea water can be motile (Grossart et al., 2001); the fractions of motile cells in this environment exhibit distinct diel and annual fluctuations that match with the known activity cycles of primary producers, and they are able to acquire a disproportionally high share of the algal-derived organic matter during bloom situations (Smriga et al., 2016).

Despite the apparent advantage of motility in a patchy environment, there are several important groups of freshwater bacteria with a permanently non-motile lifestyle, ranging from the very tiniest, 'ultramicrobacterial' morphotypes to large, filamentous forms (Hahn and Schauer, 2007). This holds true for cultivable species, e.g., affiliated with the genera *Flavobacterium* (Ali et al., 2009), *Polynucleobacter* (Hahn et al., 2009), *Limnohabitans* (Hahn et al., 2010), and Candidatus 'Methylopumilus' (Salcher et al., 2015), but also for yet uncultured taxa –as deduced from genome analysis- such as Ac1 *Actinobacteria*

(Microbacteriaceae) (Ghai et al., 2011; Ghylin et al., 2014) or LD12 *Alphaproteobacteria* (candidate family *Pelagibacteraceae*) (Zaremba-Niedzwiedzka et al., 2013; Eiler et al., 2016). Taken together, the non-motile bacteria may in fact form the larger part of the cell numbers or biomass of the free-living bacterioplankton in freshwater lakes (Pernthaler et al., 2004; Allgaier and Grossart, 2006; Salcher et al., 2008; Jezberova et al., 2010; Šimek et al., 2010; Salcher et al., 2011a; Heinrich et al., 2013). This success may reflect the trade-off between the costs and benefits of motility in a turbulent environment (Taylor and Stocker, 2012). The non-motile lifestyle is, moreover, believed to be particularly advantageous during non-bloom periods when algal-derived substrates 'hotspots' are rare (Smriga et al., 2016). Refining the above dichotomy, Hahn and co-workers have recently coined the term 'passive' lifestyle to more comprehensively describe the ecological strategy of successful freshwater species such as *P. asymbioticus or P. duraque* that are not capable of exploiting substrate heterogeneities (Hahn et al., 2012; Hahn et al., 2016a). The concept of a passive lifestyle encompasses a number of genomic adaptations besides the lack of motility, such as the absence of a chemotactic or quorum sensing system and a reduced perception of environmental stimuli.

Dissolved organic matter and nutrients

A strong albeit partially indirect case for both, competition and niche separation between lacustrine microbes can be made from the properties of the substrate and nutrient field. Freshwater DOC comprises a large range of chemical structures (Kellerman et al., 2015), and there is a relatively high and rather invariant background of rather degradation resistant compounds of allegedly terrestrial origin (Pace et al., 2004), such as humic and fulvic acids (McKnight et al., 2001). The concentration of such recalcitrant DOC is rather constant throughout the year; it typically ranges around 1-3 mg/L in clear water lakes but can be substantially higher in boreal aquatic habitats with high allochthonous influx (Tsuda et al., 2016). The recalcitrant DOC pool is composed of hundreds to thousands of individual compounds (Gonsior et al., 2013) and its turnover is low (Münster, 1993). Only between <10 and 25% of DOC is considered labile, i.e. directly accessible to rapid microbial consumption (Münster, 1993; Sondergaard and Middelboe, 1995). Within this labile pool, there are nM concentrations of low molecular weight (LMW) organic compounds such as glycolate, dissolved free amino acids or neutral aldoses that are believed to originate predominantly from the autochthonous primary production (exudation) or from microbial degradation of macromolecules (Baines and Pace, 1991; Simon et al., 2002; Paver and Kent, 2010; Sarmento et al., 2013). More recently, this view has been challenged by direct measurements of labile DOC influx from the terrestrial realms (Berggren et al., 2010; Aryal et al., 2016). Due

to rapid microbial release and consumption, these labile DOC components have high turnover rates in the range of hours to days (Simon, 1998; Weiss and Simon, 1999; Horňák and Pernthaler, 2014). Interestingly, the input of labile organic matter may lead to increased mineralization of the more recalcitrant organic matter in aquatic systems by 1-2 orders of magnitude (Guenet et al., 2010). This effect has been termed 'priming'; it seems to suggest that bacteria need the former DOC species to obtain energy for the utilization of the latter. In fact, there is recent evidence that the autochthonous labile organic C in some freshwater systems may mainly drive microbial respiration, whereas bacterial biomass predominantly consists of -arguably more recalcitrant- C of terrestrial origin (Guillemette et al., 2016).

Not all DOC components are, however beneficial for microbial growth. Secondary metabolites acting as antibiotics may be released by competing freshwater bacteria (Terkina et al., 2006; Barros et al., 2013), thereby discriminating between ecologically defined co-localized 'social cohesive units' of genotypes with common resistance patterns (Cordero et al., 2012). In addition, there are allelopathic substances released by eukaryotic phytoplankton (e.g., chrysophytes) that negatively affect bacterial growth (Hansen, 1973; Blom and Pernthaler, 2010). This chemical warfare is by no means once-sided; many freshwater bacteria exhibit algicidal properties that may be directed to particular phytoplankton species (Manage et al., 2000; Kang et al., 2005). Bacterial growth in freshwaters may also be limited by other nutritional requirements, e.g., phosphorus (P) (Vadstein, 2000; Carlsson and Caron, 2001; Smith and Prairie, 2004), to the extent that unutilized labile DOC may even accumulate under P limitation (Vadstein et al., 2003). Accordingly, freshwater microbes have developed unusual physiological strategies to efficiently grow on trace amounts of P, such as small genomes with medium to low GC content (Hahn et al., 2012; Ghylin et al., 2014; Salcher et al., 2015; Eiler et al., 2016), an extremely low RNA content, or modified membrane lipids (Yao et al., 2016). Single bacterial strains may be specialized for either pulsed or residual P availability (Vadstein, 1998), and there are clear differences between major freshwater bacterial lineages in their growth response to P addition (Šimek et al., 2006; Salcher et al., 2007).

Substrate specialists vs. generalists

Much of our knowledge about the apparent competition between individual microbial actors stems from short-term experimental enrichments (Sarmento et al., 2013; Neuenschwander et al., 2015; Paver et al., 2015; Canelhas et al., 2016). Such growth scenarios typically select for bacterial genotypes that most rapidly form biomass on the provided (labile) C source (Eilers et al., 2000; Burkert et al., 2003), indicating that these taxa

may largely ignore the recalcitrant DOC. This growth strategy, moreover, appears to be associated with a rather generalist exploitation of the surplus DOC sources (Canelhas et al., 2016). In fact, chemostat experiments with glucose-limited 'hungry' (Ferenci, 2001) *E.coli* show that these -arguably copiotrophic- microbes will maintain a low-level ability to incorporate a range of LMW DOM compounds even in their absence (Ihssen and Egli, 2005). This was interpreted as a 'preparedness' for growth as generalists under poor substrate conditions (Egli, 2010). Experiments in complex microbial model systems, moreover, suggest that assemblages of generalists can be more productive and more stable in a fluctuating environment than specialists (Matias et al., 2013).

Thus, it seems rather counterintuitive that oligotrophic environments such as the pelagic zone of freshwaters should select for bacterial substrate specialists. However, there are distinct seasonal growth patterns of different 'opportunistic' bacterial taxa in dilution or enrichment cultures (Newton and McMahon, 2011), e.g. of *Flavobacteriaceae (Neuenschwander et al., 2015)*, indicating that there is an ever changing pool of labile DOC compounds that are consumed by substrate specialists. *Flavobacteriaceae* that thrive in coastal marine waters during phytoplankton blooms express specific degradation genes for algal polysaccharides in combination with matching transporter systems for oligosaccharides (Teeling et al., 2012), pointing at niche separation via substrate specialization. Moreover, field data of sympatric bacterioplankton populations (Buck et al., 2009; Salcher et al., 2013) and genomic analyses (Hahn et al., 2012; Ghylin et al., 2014; Salcher et al., 2015; Denef et al., 2016; Eiler et al., 2016) both suggest that various aquatic bacteria exhibit a conspicuous extent of specialization for particular LMW DOM compounds, or for DOM derived from particular algae (Šimek et al., 2011; Sarmento et al., 2013).

Adaptations other than substrate generalism might be beneficial in a growth-limiting oligotrophic environment that at the same time is also highly heterogeneous. For example, it is conceivable that some bacteria are constitutively prepared to incorporate particular substrates at extremely fast rates across large concentration ranges, even if these substrates are only sporadically available at high concentrations: LD12 *Alphaproteobacteria* were more effective in the uptake of glutamine than the community average both at 1 and 10 nM concentration after only 15 min of incubation (Salcher et al., 2011a). 80% of Candidatus Aquirestis calciphila (*Saprospiraceae* of the LD2 lineage), but <10% of all bacteria readily incorporated N-acetyl glucosamine offered at 20 nM (Eckert et al., 2013), although the concentrations of this substrate were <1 nM in the vast majority of samples from this lake (Horňák and Pernthaler, 2014). A large fraction of *Polynucleobacter* spp. incorporated radiolabeled acetate added at nM concentrations against a thousand fold higher natural background of this substrate, hinting at extremely high uptake velocity (Buck et al., 2009). A

'predictive targeting' (bet hedging) of a subset of key substrates across concentrations ranges that match environmental fluctuations by oligocarbophilic bacteria is also suggested by the high frequency of transporter genes for nitrogenous compounds, including amino acids, in the highly streamlined genome of SAR11 (candidate family Pelagibacteraceae, the marine sister group of freshwater LD12 *Alphaproteobacteria* (Eiler et al., 2016)) and the disproportionally high abundance of such transporters in the SAR11 proteome at oligotrophic conditions (Giovannoni et al., 2005; Sowell et al., 2009).

Another angle for interpreting the contrasting strategies of substrate generalists and specialists is provided by the conceptual framework of 'public' vs. 'private goods' (Bachmann et al., 2016): If a common resource such as dissolved amino acids is to be shared between many microbial competitors (Salcher et al., 2013; Canelhas et al., 2016), a maximization of growth rates (Šimek et al., 2005), albeit wasteful, is regarded as the best metabolic strategy. By contrast, bacteria that monopolize a particular substrate, e.g., the methylotrophic betaproteobacteria (Salcher et al., 2015), are expected to be optimized for growth yield. Finally, there are numerous microbially generated products that are shared between populations (Morris, 2015). The apparent loss of essential synthetic functions in some specialized freshwater bacteria with streamline genomes (Eiler et al., 2016) in combination with the 'leakiness' of others for organic compounds and vitamins (Kawasaki and Benner, 2006; Garcia et al., 2015) thus adds another layer of complexity to their substrate-related interactions.

Tansley's rabbits and other killers of winners

The grazing by free-living nano-sized flagellated protists ranks amongst the most important sources of mortality for freshwater bacteria (Sanders et al., 1989), and their competitive interactions are profoundly altered in the presence of predators (Salcher et al., 2016). Predation, moreover, directly selects for or against the occurrence of particular bacterial pheno- and/ or genotypes (Jürgens and Matz, 2002; Pernthaler, 2005). The second major 'top-down' control on freshwater bacterioplankton is mediated through viral lysis ((Weinbauer, 2004; Middelboe et al., 2008) and references therein). Viral mortality is believed to act more specifically than predation on individual bacterial genotypes by targeting cell surface epitopes rather than broad phenotypic categories (Winter et al., 2010). Nevertheless, the host ranges of aquatic phages may also differ in size and/or partially overlap (Holmfeldt et al., 2007).

Selective protistan foraging and strain-specific viral lysis have consequences for the competition between bacterial populations: (i) The indirect 'physiological profiling' of bacteria by protistan grazing of large, active cells (Del Giorgio et al., 1996) leads to a negative

frequency-dependent selection on rapidly dividing bacterial populations that is reminiscent of an observation by botanists in the early 20th century (Tansley and Adamson, 1925): The fencing out of rabbits from plots of land led to a 'very great diminution of the number of individual plants […]' except for a single species 'which increased enormously'. In analogy with these findings, the removal of protistan predators from aquatic microbial assemblages tends to favour the growth of a few rapidly growing genotypes that are otherwise suppressed (Beardsley et al., 2003; Šimek et al., 2005; Salcher et al., 2007). (ii) A somewhat similar concept, albeit derived from theoretical considerations, has originated from viral ecology (Thingstad, 2000; Winter et al., 2010): The 'killing the winner' (KtW) model predicts, amongst other things, that the strains with the greatest 'bottom-up' competitive abilities and no or little investment in defence will suffer the highest losses by viral lysis, thereby maintaining overall community diversity. The empirical testing of KtW is somewhat constraint by its self-imposed assumptions, such as steady state conditions, a single substrate source and a homogenous environment (Thingstad, 2000). However, more recent conceptual refinements, such as the inclusion of host resistance costs have succeeded in reproducing observed abundance patterns of bacterial taxa and their viruses (Vage et al., 2013).

The simultaneous presence of grazers and viruses increases both, overall prokaryotic and viral activity, as compared to either single factor, likely due to the concerted release of DOM and nutrients (Šimek et al., 2001; Ram and Sime-Ngando, 2014). Since both mortality sources most strongly affect populations of 'growth specialists', such bacteria will disproportionally contribute to the carbon transfer to higher trophic levels (Zeder et al., 2009; Šimek et al., 2014), and possibly also to the recycling of nutrients (Caron et al., 1988; Riemann et al., 2009). On the other hand, aquatic bacteria rapidly develop resistance to phages (Middelboe et al., 2009) and feature a range of phenotypic adaptations against protistan foraging (Šimek and Chrzanowski, 1992; Matz and Jürgens, 2005; Tarao et al., 2009; Blom et al., 2010), thereby engaging in a physiological trade-off between growth and defence-related traits (Middelboe et al., 2009; Winter et al., 2010; Baumgartner et al., 2016). Some predation or phage resistant bacteria even appear to derive a benefit from the consumption or lysis of more vulnerable taxa that goes beyond the reduced competition for public goods (Šimek et al., 2007). This might be due to the specialization on the additional substrates that are released by mortality, e.g. derived from cell wall fragments (Eckert et al., 2013).

In fact, a large proportion or even the majority of freshwater bacterioplankton biomass may be allocated to groups that are partially or fully protected from protistan grazing (Pernthaler et al., 2004; Salcher et al., 2010): For one, pelagic communities transiently harbour substantial numbers of protist-inedible filamentous bacterial morphotypes from various phylogenetic groups (Jürgens et al., 1999), whereas such threadlike bacteria are typically

absent in coastal or offshore marine habitats. This difference cannot solely be explained by the contrasting availability of DOC or nutrients in the two biomes, since the habitat range of filamentous freshwater bacteria encompasses hypertrophic ponds (Sommaruga, 1995), meso- to eutrophic systems (Pernthaler et al., 2004; Schauer et al., 2005), but also ultraoligotrophic high mountain lakes (Pernthaler et al., 1998). Secondly, large populations of minute gram-positive bacteria with highly reduced genomes (Ghylin et al., 2014) are found in the pelagic zone of fresh and brackish waters with contrasting trophic state and water chemistry (Warnecke et al., 2005; Allgaier and Grossart, 2006; Newton et al., 2007; Holmfeldt et al., 2009; Andersson et al., 2010; Ghai et al., 2011; Piwosz et al., 2013). These acI *Actinobacteria* are believed to resist protistan predation due to their smaller than average cell size (Pernthaler et al., 2001; Salcher et al., 2010), and potentially also due to their specific cell wall and/or surface properties, as has been shown in another freshwater actinobacterial strain from the Luna lineage (*Microbacteriaceae)* (Tarao et al., 2009).

Conclusions:

This review sacrifices completeness for breadth, with a tendency of focussing on the rather recent literature, and the author excuses to all specialists of the various here discussed topics if my account appears overly simplistic. It was my intention to present the diversity of interesting perspectives on the subject, and to highlight the value of all these different angles for understanding the interactions between freshwater bacteria and their environment. This may sometimes be lost in the unifying waves of methodological advance. I, moreover, take a somewhat 'Hutchinsonian' viewpoint (Hutchinson, 1961) by implying that the intrinsic variability of the habitat and the sharing of multiple resources create the stage for microbial coexistence. There are other, equally valid perspectives, e.g., nested predator-prey and parasite-host interactions across a range of phylogenetic levels have been suggested to generate complexity in microbial communities even at uniform, steady state conditions (Vage and Thingstad, 2015). In any case, it is likely that pelagic freshwater bacteria are also confronted with the universal ecological dilemma of succeeding in an environment that is riddled with stochasticity using a toolbox of largely deterministic components such as gene products and biochemical pathways.

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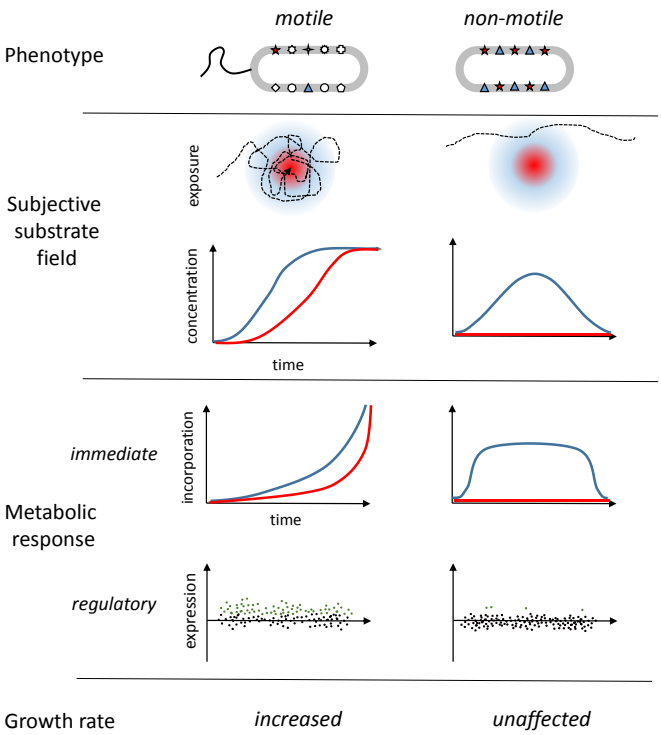
Figure legends:

Figure 1: Conceptual depiction of the different response of motile and non-motile freshwater bacteria to substrates with microscale patchiness. In this concept, motile bacteria feature a large range of different transporters that are expressed at low levels even in the absence of the stimulus, whereas non-motile forms only possess transporters for a selected substrate range, albeit in high abundance. Thus, the latter will have an advantage in the instantaneous consumption of a targeted substrate. Motile bacteria will attempt to chemotactically approach the source and in doing so may encounter additional substrate types, whereas non-motile cells are passively exposed to substrate flutuations. Accordingly, motile bacteria will interpret the conditions as favourable for a general upshift of cell metabolism, eventually leading to higher growth rates. By contrast, non-motile bacteria will not be able to predict future growth conditions from a single case of substrate fluctuation and their metabolic response to it will be more limited.


motile
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immediate
incorporation
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Metabolic response
regulatory
expression
Growth rate
increased
unaffected